

in IDS

LOCUS AF186371 3014 bp DNA linear BCT 10-SEP-2002  
DEFINITION Streptomyces coelicolor A3(2) AhpD (ahpD), AhpC (ahpC), and OxyR (oxyR) genes, complete cds.  
ACCESSION AF186371  
VERSION AF186371.1 GI:6288864  
SOURCE Streptomyces coelicolor A3(2)  
ORGANISM Streptomyces coelicolor A3(2)  
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
Streptomycineae; Streptomycetaceae; Streptomyces.  
REFERENCE 1 (bases 1 to 3014)  
AUTHORS Hahn, J.S., Oh, S.Y. and Roe, J.H.  
TITLE Role of OxyR as a Peroxide-Sensing Positive Regulator in  
Streptomyces coelicolor A3(2)  
JOURNAL J. Bacteriol. 184 (19), 5214-5222 (2002)  
MEDLINE 22206464  
PUBMED 12218006  
REFERENCE 2 (bases 1 to 3014)  
AUTHORS Hahn, J.-S. and Roe, J.-H.  
TITLE Role of OxyR as a regulator of the ahpCD operon encoding alkyl  
hydroperoxide reductase system in Streptomyces coelicolor  
JOURNAL Unpublished  
REFERENCE 3 (bases 1 to 3014)  
AUTHORS Hahn, J.-S. and Roe, J.-H.  
TITLE Direct Submission  
JOURNAL Submitted (15-SEP-1999) Microbiology, Seoul National University,  
Kwan-Ak Gu, Shin-Lim 9Dong, San 56-1, Seoul 151-742, Korea

Query Match 13.0%; Score 217.2; DB 1; Length 3014;  
Best Local Similarity 53.6%; Pred. No. 2.8e-43;  
Matches 478; Conservative 0; Mismatches 408; Indels 6; Gaps 1;

Qy	492	TGAGCAATAAAGAGTACCGGGCCACACTCGCCCAGCTCGCACCTTGTCAACCATCGCAG	551
Db	1826	TGTCCAGTAAGAAGAGACAGGCCAGCCTCGCTCAGCTGCAGGGCTTCCGACGCGGTCGCCG	1885
Qy	552	AATGCAAGCACTTGGTACTGCTGCCACCAAGCTGTCCATTTCGCAGCCATCCCTCTCCC	611
Db	1886	AGCACCTGCACTTCCGTACGCCGCCGCCGCGATCGGCATGAGCCAGGCCGGCGCTCTCGG	1945
Qy	612	AGGCACTTGTCGCATTAGAAACAGGCCTGGGAGTTCACTGATGAAACGCTCCACCCGCA	671
Db	1946	GTGCCGTTCCGCCCTGGAAGAGGCACTGGGTCTCACCCCTCTGGGGCGTACGACGCCA	2005
Qy	672	AGGTCAATTGTCACCCCCAGCGGGCGAGAAGTTGCTGCCATTGCCAAATCCACCCCTGACG	731
Db	2006	AGGTGCTGCTGTCCCCGGCCGGCGCACGGCTCGCGGTGCGGACCAAGGCGGTACTGGCGG	2065
Qy	732	CGGCGGAGTCTTCCTCTCCACGCCAACGGCGCCAACGGTTCGCTCACTGGACCGTTGA	791
Db	2066	AGGTGGCGCGCTCGTGAGGGAGGCGGAGGCGGTGCGGGCGCCCTCACCGCGCGCTGC	2125
Qy	792	CCGTAGGCATCATCCCCACGGCGCTCCTTACATTGCGTCAATGCTGTCCATCGTGG	851
Db	2126	GGCTCGGCGTCATCCGACCGTGGCGCCGTATGTGCTGCCGACGGTGCTGCGCCTCGTCC	2185
Qy	852	ATGAAGAATATCCAGATCTGGAACCTCACATCGTCAGGGACCAAACCAAGCATCTTCTCG	911

Db	2186	ACGAGCGCTATCCGACCTCGACCTCCAGGTCCACGAGGAGCAGACGGCGAGCCTCCTGG	2245
Qy	912	CGTTGCTGCGCGACGGCGCCATCGACGTCGCCATGATGGCCCTGCCTCTGAGGCACCAG	971
Db	2246	AGGGCCTGACGACCGGCGGCTCGACCTGCTGCTGCTCGCGGTGCCCTCGCGTCCCCG	2305
Qy	972	GCATGAAGGAAATCCCCCTCTACGACGAAGACTTTATCGTCGTTACAGCTAGCGATCAC	1031
Db	2306	GCGTCACCGAACCTCCGCTCTCGACGAGGACTTCGTCCTGGTCACGCCGCTCGACCA	2365
Qy	1032	CCTTCGCCGGGCCAAGACTTAGAACTATCCGCCTTAGAAGACCTCGATCTGCTGCTTC	1091
Db	2366	GAECTGGCGGGCCGGGAGGGCCTGGAGCGCTCGGTGCTGCGCGAGCTGAAGCTGCTG	2425
Qy	1092	TCGACGACGGACACTGCCTCACGACCAAATTGTGGACCTGTGCCGCCGGAGACATCA	1151
Db	2426	TCGACGAGGGGACTGCCTCGCGACCAAGCGCTCGACATCTGCC-----GGGAGGC	2479
Qy	1152	ACCCCATTAGCTCCACTACTGCTGTCACCCGCGCATCCAGCCTTACCAACCGTCATGCAGC	1211
Db	2480	GCGCGCGGGGGTCCCGCGACGACGACCAACGGCCGCCGGTCTGTCGACGCTGGTACAGC	2539
Qy	1212	TCGTCGTCGCCGGCCTTGGATCCACCTGGTCCAATCAGCGCAATCCATGGGATGCA	1271
Db	2540	TGGTGGCGGGCGGCCCTCGGGGTGACGCTGCTGCCCGCACCGCCGTCCGGTGGAGACCT	2599
Qy	1272	CCCGACCAGGACTGGCAACAGCCAATTCAACTCTGATGTCACCGCAAACCGCCGCATTG	1331
Db	2600	CCCGCTCCAGCCAGCTCCTCACCGCGTCTTCACCGACCCGGCCCCACCCGCCGTATCG	2659
Qy	1332	GÄTTGGTGTACCGTTCTCTTCTCGCGCCGAAGAGTTCGAACAGTTGC	1383
Db	2660	CCCTCGCCATGCGCACGGCGCGGCCGCTCGGCGGAGTACGGGAACGGC	2711